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OIIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/847,010

DATE: 05/15/2001
 TIME: 15:18:15

Input Set : A:\Frey.app
 Output Set: N:\CRF3\05152001\I847010.raw

3 <110> APPLICANT: FREY, Perry A.
 4 RUZICKA, Frank J.
 6 <120> TITLE OF INVENTION: DNA MOLECULES ENCODING BACTERIAL LYSINE 2,3-AMINOMUTASE
 8 <130> FILE REFERENCE: 032026/0476
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/847,010
 C--> 11 <141> CURRENT FILING DATE: 2001-05-01
 13 <150> PRIOR APPLICATION NUMBER: US 09/198,942
 14 <151> PRIOR FILING DATE: 1998-11-24
 16 <160> NUMBER OF SEQ ID NOS: 32
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1251
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Clostridium subterminale
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(1248)
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 32 1 5 10 15
 34 tgg aat gac tgg aga tgg caa gta aga aac aga ata gaa act gtt gaa 96
 35 Trp Asn Asp Trp Arg Trp Gln Val Arg Asn Arg Ile Glu Thr Val Glu
 36 20 25 30
 38 gaa cta aag aaa tac ata cca tta aca aaa gaa gaa gaa gaa gga gta 144
 39 Glu Leu Lys Lys Tyr Ile Pro Leu Thr Lys Glu Glu Glu Glu Gly Val
 40 35 40 45
 42 gct caa tgt gta aaa tca tta aga atg gct att act cca tat tat cta 192
 43 Ala Gln Cys Val Lys Ser Leu Arg Met Ala Ile Thr Pro Tyr Tyr Leu
 44 50 55 60
 46 tca tta atc gat cct aac gat cct aat gat cca gta aga aaa caa gct 240
 47 Ser Leu Ile Asp Pro Asn Asp Pro Asn Asp Pro Val Arg Lys Gln Ala
 48 65 70 75 80
 50 att cca aca gca tta gag ctt aac aaa gct gct gca gat ctt gaa gac 288
 51 Ile Pro Thr Ala Leu Glu Leu Asn Lys Ala Ala Ala Asp Leu Glu Asp
 52 85 90 95
 54 cca tta cat gaa gat aca gat tca cca gta cct gga tta act cac aga 336
 55 Pro Leu His Glu Asp Thr Asp Ser Pro Val Pro Gly Leu Thr His Arg
 56 100 105 110
 58 tat cca gat aga gta tta tta tta ata act gat atg tgc tca atg tac 384
 59 Tyr Pro Asp Arg Val Leu Leu Ile Thr Asp Met Cys Ser Met Tyr
 60 115 120 125
 62 tgc aga cac tgt aca aga aga aga ttt gca gga caa agc gat gac tct 432
 63 Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Ser Asp Asp Ser
 64 130 135 140
 66 atg cca atg gaa aga ata gat aaa gct ata gat tat atc aga aat act 480
 67 Met Pro Met Glu Arg Ile Asp Lys Ala Ile Asp Tyr Ile Arg Asn Thr

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74 tct gat gaa aca tta gaa tac atc ata gct aaa tta aga gaa ata cca 576
75 Ser Asp Glu Thr Leu Glu Tyr Ile Ile Ala Lys Leu Arg Glu Ile Pro
76          180          185          190
78 cac gtt gaa ata gta aga ata ggt tca aga act cca gtt gtt ctt cca 624
79 His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu Pro
80          195          200          205
82 caa aga ata act cca gaa ctt gta aat atg ctt aaa aaa tat cat cca 672
83 Gln Arg Ile Thr Pro Glu Leu Val Asn Met Leu Lys Lys Tyr His Pro
84          210          215          220
86 gta tgg tta aac act cac ttt aac cat cca aat gaa ata aca gaa gaa 720
87 Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Glu
88 225          230          235          240
90 tca act aga gct tgt caa tta ctt gct gac gca gga gta cct cta gga 768
91 Ser Thr Arg Ala Cys Gln Leu Leu Ala Asp Ala Gly Val Pro Leu Gly
92          245          250          255
94 aac caa tca gtt tta tta aga gga gtt aac gat tgc gta cac gta atg 816
95 Asn Gln Ser Val Leu Leu Arg Gly Val Asn Asp Cys Val His Val Met
96          260          265          270
98 aaa gaa tta gtt aac aaa tta gta aaa ata aga gta aga cct tac tac 864
99 Lys Glu Leu Val Asn Lys Leu Val Lys Ile Arg Val Arg Pro Tyr Tyr
100          275          280          285
102 atc tat caa tgt gac tta tca tta gga ctt gag cac ttc aga act cca 912
103 Ile Tyr Gln Cys Asp Leu Ser Leu Gly Leu Glu His Phe Arg Thr Pro
104          290          295          300
106 gtt tct aaa ggt atc gaa atc att gaa gga tta aga gga cat act tca 960
107 Val Ser Lys Gly Ile Glu Ile Ile Glu Gly Leu Arg Gly His Thr Ser
108 305          310          315          320
110 gga tac tgc gta cca aca ttc gtt gtt gac gct cca ggt ggt ggt gga 1008
111 Gly Tyr Cys Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly Gly
112          325          330          335
114 aaa aca cca gtt atg cca aac tac gtt att tca caa agt cat gac aaa 1056
115 Lys Thr Pro Val Met Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys
116          340          345          350
118 gta ata tta aga aac ttt gaa ggt gtt ata aca act tat tca gaa cca 1104
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120          355          360          365
122 ata aac tat act cca gga tgc aac tgt gat gtt tgc act ggc aag aaa 1152
123 Ile Asn Tyr Thr Pro Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys
124          370          375          380
126 aaa gtt cat aag gtt gga gtt gct gga tta tta aac gga gaa gga atg 1200
127 Lys Val His Lys Val Gly Val Ala Gly Leu Leu Asn Gly Glu Gly Met
128 385          390          395          400
130 gct cta gaa cca gta gga tta gag aga aat aag aga cac gtt caa gaa 1248
131 Ala Leu Glu Pro Val Gly Leu Glu Arg Asn Lys Arg His Val Gln Glu
132          405          410          415

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134 taa 1251

137 <210> SEQ ID NO: 2

138 <211> LENGTH: 416

139 <212> TYPE: PRT

140 <213> ORGANISM: Clostridium subterminale

142 <400> SEQUENCE: 2

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146 Trp Asn Asp Trp Arg Trp Gln Val Arg Asn Arg Ile Glu Thr Val Glu

147 20 25 30

149 Glu Leu Lys Lys Tyr Ile Pro Leu Thr Lys Glu Glu Glu Glu Gly Val

150 35 40 45

152 Ala Gln Cys Val Lys Ser Leu Arg Met Ala Ile Thr Pro Tyr Tyr Leu

153 50 55 60

155 Ser Leu Ile Asp Pro Asn Asp Pro Asn Asp Pro Val Arg Lys Gln Ala

156 65 70 75 80

158 Ile Pro Thr Ala Leu Glu Leu Asn Lys Ala Ala Ala Asp Leu Glu Asp

159 85 90 95

161 Pro Leu His Glu Asp Thr Asp Ser Pro Val Pro Gly Leu Thr His Arg

162 100 105 110

164 Tyr Pro Asp Arg Val Leu Leu Leu Ile Thr Asp Met Cys Ser Met Tyr

165 115 120 125

167 Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Ser Asp Asp Ser

168 130 135 140

170 Met Pro Met Glu Arg Ile Asp Lys Ala Ile Asp Tyr Ile Arg Asn Thr

171 145 150 155 160

173 Pro Gln Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu Val

174 165 170 175

176 Ser Asp Glu Thr Leu Glu Tyr Ile Ile Ala Lys Leu Arg Glu Ile Pro

177 180 185 190

179 His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu Pro

180 195 200 205

182 Gln Arg Ile Thr Pro Glu Leu Val Asn Met Leu Lys Lys Tyr His Pro

183 210 215 220

185 Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Ile Thr Glu Glu

186 225 230 235 240

188 Ser Thr Arg Ala Cys Gln Leu Leu Ala Asp Ala Gly Val Pro Leu Gly

189 245 250 255

191 Asn Gln Ser Val Leu Leu Arg Gly Val Asn Asp Cys Val His Val Met

192 260 265 270

194 Lys Glu Leu Val Asn Lys Leu Val Lys Ile Arg Val Arg Pro Tyr Tyr

195 275 280 285

197 Ile Tyr Gln Cys Asp Leu Ser Leu Gly Leu Glu His Phe Arg Thr Pro

198 290 295 300

200 Val Ser Lys Gly Ile Glu Ile Ile Glu Gly Leu Arg Gly His Thr Ser

201 305 310 315 320

203 Gly Tyr Cys Val Pro Thr Phe Val Val Asp Ala Pro Gly Gly Gly Gly

204 325 330 335

206 Lys Thr Pro Val Met Pro Asn Tyr Val Ile Ser Gln Ser His Asp Lys

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210          355          360          365
212 Ile Asn Tyr Thr Pro Gly Cys Asn Cys Asp Val Cys Thr Gly Lys Lys
213          370          375          380
215 Lys Val His Lys Val Gly Val Ala Gly Leu Leu Asn Gly Glu Gly Met
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223 <211> LENGTH: 1029
224 <212> TYPE: DNA
225 <213> ORGANISM: Escherichia coli
227 <220> FEATURE:
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229 <222> LOCATION: (1)..(1026)
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234 1          5          10          15
236 acg caa ctt gcc gat gtt gtg acc gat cct gat gaa ctt ctg cgt ctt 96
237 Thr Gln Leu Ala Asp Val Val Thr Asp Pro Asp Glu Leu Leu Arg Leu
238          20          25          30
240 ttg aat ata gac gcg gag gaa aaa ctg tta gcc gga cgc agc gcc aaa 144
241 Leu Asn Ile Asp Ala Glu Glu Lys Leu Leu Ala Gly Arg Ser Ala Lys
242          35          40          45
244 aag ctt ttt gcc ctg cgt gtg ccc cgc tca ttt atc gat cgc atg gag 192
245 Lys Leu Phe Ala Leu Arg Val Pro Arg Ser Phe Ile Asp Arg Met Glu
246          50          55          60
248 aaa ggc aat ccg gac gat cct ctt ttg cgt cag gta ctt acc tcg caa 240
249 Lys Gly Asn Pro Asp Asp Pro Leu Leu Arg Gln Val Leu Thr Ser Gln
250 65          70          75          80
252 gat gag ttt gtc atc gcg ccc gga ttc tcc acc gac cca ctg gaa gaa 288
253 Asp Glu Phe Val Ile Ala Pro Gly Phe Ser Thr Asp Pro Leu Glu Glu
254          85          90          95
256 cag cac agc gta gtg cct ggt ttg ttg cat aaa tac cac aac cgg gcg 336
257 Gln His Ser Val Val Pro Gly Leu Leu His Lys Tyr His Asn Arg Ala
258          100          105          110
260 ctt ttg ctg gtc aaa ggc ggc tgc gcg gta aat tgc cgc tat tgc ttc 384
261 Leu Leu Leu Val Lys Gly Gly Cys Ala Val Asn Cys Arg Tyr Cys Phe
262          115          120          125
264 cgt cgt cac ttc ccc tat gcc gaa aat cag ggc aac aag cgt aac tgg 432
265 Arg Arg His Phe Pro Tyr Ala Glu Asn Gln Gly Asn Lys Arg Asn Trp
266          130          135          140
268 caa act gca ctt gag tat gtt gct gcg cat ccg gaa ctg gac gag atg 480
269 Gln Thr Ala Leu Glu Tyr Val Ala Ala His Pro Glu Leu Asp Glu Met
270 145          150          155          160
272 att ttc tcc ggc ggc gat ccg ctg atg gcg aaa gat cac gag ctg gac 528
273 Ile Phe Ser Gly Gly Asp Pro Leu Met Ala Lys Asp His Glu Leu Asp

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274          165          170          175
276 tgg ttg ctc aca caa ctg gaa gcc atc ccg cat ata aaa cgt ctg cgg 576
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278          180          185          190
280 att cac agc cgt ctg ccg att gtg atc ccg gca cgt atc acc gag gcg 624
281 Ile His Ser Arg Leu Pro Ile Val Ile Pro Ala Arg Ile Thr Glu Ala
282          195          200          205
284 ctg gtt gaa tgc ttt gcc cgt tct acg ctg caa atc ttg ctg gtg aat 672
285 Leu Val Glu Cys Phe Ala Arg Ser Thr Leu Gln Ile Leu Leu Val Asn
286          210          215          220
288 cac atc aac cat gcc aat gag gta gat gaa aca ttc cgt cag gcg atg 720
289 His Ile Asn His Ala Asn Glu Val Asp Glu Thr Phe Arg Gln Ala Met
290 225          230          235          240
292 gct aag ttg cgc cgg gta ggc gtt act ttg ctg aac cag agc gtt ctg 768
293 Ala Lys Leu Arg Arg Val Gly Val Thr Leu Leu Asn Gln Ser Val Leu
294          245          250          255
296 tta cgt gat gtg aac gat aac gca caa acg ctg gca aac ctg agt aat 816
297 Leu Arg Asp Val Asn Asp Asn Ala Gln Thr Leu Ala Asn Leu Ser Asn
298          260          265          270
300 gcg ttg ttc gat gcc ggc gta atg ccg tat tac ctg cat gtg ctc gat 864
301 Ala Leu Phe Asp Ala Gly Val Met Pro Tyr Tyr Leu His Val Leu Asp
302          275          280          285
304 aaa gta cag ggc gcg gcg cat ttt atg gtg agt gat gac gaa gca cgg 912
305 Lys Val Gln Gly Ala Ala His Phe Met Val Ser Asp Asp Glu Ala Arg
306          290          295          300
308 cag att atg cgt gag ttg ctg aca ctg gtg tcg gga tat ctg gtg ccg 960
309 Gln Ile Met Arg Glu Leu Leu Thr Leu Val Ser Gly Tyr Leu Val Pro
310 305          310          315          320
312 aaa ctg gcg cga gaa att ggc ggc gaa ccc agc aaa acg ccg ctg gat 1008
313 Lys Leu Ala Arg Glu Ile Gly Gly Glu Pro Ser Lys Thr Pro Leu Asp
314          325          330          335
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322 <211> LENGTH: 342
323 <212> TYPE: PRT
324 <213> ORGANISM: Escherichia coli
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330 Thr Gln Leu Ala Asp Val Val Thr Asp Pro Asp Glu Leu Leu Arg Leu
331 20 25 30
333 Leu Asn Ile Asp Ala Glu Glu Lys Leu Leu Ala Gly Arg Ser Ala Lys
334 35 40 45
336 Lys Leu Phe Ala Leu Arg Val Pro Arg Ser Phe Ile Asp Arg Met Glu
337 50 55 60
339 Lys Gly Asn Pro Asp Asp Pro Leu Leu Arg Gln Val Leu Thr Ser Gln
340 65 70 75 80

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Please Note:

Use f n and/ r Xaa have been detected in the Sequence Listing. Please review the Sequence Listing t ensure that a c rresp nding explanation is pres nted in th <220> to <223> fields of each sequence which presents at least ne n r Xaa.

VERIFICATION SUMMARY DATE: 05/15/2001
PATENT APPLICATION: US/09/847,010 TIME: 15:18:16

Input Set : A:\Frey.app
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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20